

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/590, 958  
Source: LFW0  
Date Processed by STIC: 09/05/2006

# ***ENTERED***



IFWO

## RAW SEQUENCE LISTING

DATE: 09/05/2006

PATENT APPLICATION: US/10/590,958

TIME: 15:09:03

Input Set : A:\Sequence Listing-13987-00019-US.txt

Output Set: N:\CRF4\09052006\J590958.raw

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3 <110> APPLICANT: Cirpus, Petra
4     Bauer, Jorg
5     Zank, Thorsten
6     Heinz, Ernst
8 <120> TITLE OF INVENTION: METHOD FOR PRODUCING UNSATURATED OMEGA-3-FATTY ACIDS IN
9     TRANSGENIC ORGANISMS
11 <130> FILE REFERENCE: 13987-00019-US
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/590,958
C--> 13 <141> CURRENT FILING DATE: 2006-08-25
13 <150> PRIOR APPLICATION NUMBER: PCT/EP2005/001865
14 <151> PRIOR FILING DATE: 2005-02-23
16 <150> PRIOR APPLICATION NUMBER: DE 10 2004 009 458.6
17 <151> PRIOR FILING DATE: 2004-02-27
19 <160> NUMBER OF SEQ ID NOS: 6
21 <170> SOFTWARE: PatentIn version 3.3
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 1086
25 <212> TYPE: DNA
26 <213> ORGANISM: Phytophthora infestans
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (1)..(1086)
31 <223> OTHER INFORMATION: Omega-3-desaturase
33 <400> SEQUENCE: 1
34 atg gcg acg aag gag gcg tat gtg ttc ccc act ctg acg gag atc aag      48
35 Met Ala Thr Lys Glu Ala Tyr Val Phe Pro Thr Leu Thr Glu Ile Lys
36 1           5           10           15
37 cgg tcg cta cct aaa gac tgt ttc gag gct tcg gtg cct ctg tcg ctc      96
38 Arg Ser Leu Pro Lys Asp Cys Phe Glu Ala Ser Val Pro Leu Ser Leu
39           20           25           30
40 tac tac acc gtg cgt tgt ctg gtg atc gcg gtg gct cta acc ttc ggt      144
41 Tyr Tyr Thr Val Arg Cys Leu Val Ile Ala Val Ala Leu Thr Phe Gly
42           35           40           45
43 ctc aac tac gct cgc gct ctg ccc gag gtc gag agc ttc tgg gct ctg      192
44 Leu Asn Tyr Ala Arg Ala Leu Pro Glu Val Glu Ser Phe Trp Ala Leu
45           50           55           60
46 gac gcc gca ctc tgc acg ggc tac atc ttg ctg cag ggc atc gtg ttc      240
47 Asp Ala Ala Leu Cys Thr Gly Tyr Ile Leu Leu Gln Gly Ile Val Phe
48 65           70           75           80
49 tgg ggc ttc ttc acg gtg ggc cac gat gcc ggc cac ggc gcc ttc tcg      288
50 Trp Gly Phe Phe Thr Val Gly His Asp Ala Gly His Gly Ala Phe Ser
51           85           90           95
52 cgc tac cac ctg ctt aac ttc gtg gtg ggc act ttc atg cac tcg ctc      336

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53	Arg	Tyr	His	Leu	Leu	Asn	Phe	Val	Val	Gly	Thr	Phe	Met	His	Ser	Leu	
54				100					105					110			
55	atc	ctc	acg	ccc	ttc	gag	tcg	tgg	aag	ctc	acg	cac	cgt	cac	cac	cac	384
56	Ile	Leu	Thr	Pro	Phe	Glu	Ser	Trp	Lys	Leu	Thr	His	Arg	His	His	His	
57			115					120					125				
58	aag	aac	acg	ggc	aac	att	gac	cgt	gac	gag	gtc	ttc	tac	ccg	caa	cgc	432
59	Lys	Asn	Thr	Gly	Asn	Ile	Asp	Arg	Asp	Glu	Val	Phe	Tyr	Pro	Gln	Arg	
60			130					135				140					
61	aag	gcc	gac	gac	cac	ccg	ctg	tct	cgc	aac	ctg	att	ctg	gcg	ctc	ggg	480
62	Lys	Ala	Asp	Asp	His	Pro	Leu	Ser	Arg	Asn	Leu	Ile	Leu	Ala	Leu	Gly	
63	145					150				155						160	
64	gca	gcg	tgg	ctc	gcc	tat	ttg	gtc	gag	ggc	ttc	cct	cct	cgt	aag	gtc	528
65	Ala	Ala	Trp	Leu	Ala	Tyr	Leu	Val	Glu	Gly	Phe	Pro	Pro	Arg	Lys	Val	
66				165						170					175		
67	aac	cac	ttc	aac	ccg	ttc	gag	cct	ctg	ttc	gtg	cgt	cag	gtg	tca	gct	576
68	Asn	His	Phe	Asn	Pro	Phe	Glu	Pro	Leu	Phe	Val	Arg	Gln	Val	Ser	Ala	
69			180					185					190				
70	gtg	gta	atc	tct	ctt	ctc	gcc	cac	ttc	ttc	gtg	gcc	gga	ctc	tcc	atc	624
71	Val	Val	Ile	Ser	Leu	Leu	Ala	His	Phe	Phe	Val	Ala	Gly	Leu	Ser	Ile	
72			195					200					205				
73	tat	ctg	agc	ctc	cag	ctg	ggc	ctt	aag	acg	atg	gca	atc	tac	tac	tat	672
74	Tyr	Leu	Ser	Leu	Gln	Leu	Gly	Leu	Lys	Thr	Met	Ala	Ile	Tyr	Tyr	Tyr	
75		210					215				220						
76	gga	cct	gtt	ttt	gtg	ttc	ggc	agc	atg	ctg	gtc	att	acc	acc	ttc	cta	720
77	Gly	Pro	Val	Phe	Val	Phe	Gly	Ser	Met	Leu	Val	Ile	Thr	Thr	Phe	Leu	
78	225					230				235					240		
79	cac	cac	aat	gat	gag	gag	acc	cca	tgg	tac	gcc	gac	tcg	gag	tgg	acg	768
80	His	His	Asn	Asp	Glu	Glu	Thr	Pro	Trp	Tyr	Ala	Asp	Ser	Glu	Trp	Thr	
81			245						250					255			
82	tac	gtc	aag	ggc	aac	ctc	tcg	tcc	gtg	gac	cga	tcg	tac	ggc	gcg	ctc	816
83	Tyr	Val	Lys	Gly	Asn	Leu	Ser	Ser	Val	Asp	Arg	Ser	Tyr	Gly	Ala	Leu	
84			260						265				270				
85	att	gac	aac	ctg	agc	cac	aac	atc	ggc	acg	cac	cag	atc	cac	cac	ctt	864
86	Ile	Asp	Asn	Leu	Ser	His	Asn	Ile	Gly	Thr	His	Gln	Ile	His	His	Leu	
87		275						280				285					
88	ttc	cct	atc	att	ccg	cac	tac	aaa	ctc	aag	aaa	gcc	act	gcg	gcc	ttc	912
89	Phe	Pro	Ile	Ile	Pro	His	Tyr	Lys	Leu	Lys	Lys	Ala	Thr	Ala	Ala	Phe	
90		290					295				300						
91	cac	cag	gct	ttc	cct	gag	ctc	gtg	cgc	aag	agc	gac	gag	cca	att	atc	960
92	His	Gln	Ala	Phe	Pro	Glu	Leu	Val	Arg	Lys	Ser	Asp	Glu	Pro	Ile	Ile	
93	305					310				315					320		
94	aag	gct	ttc	ttc	cgg	gtt	gga	cgt	ctc	tac	gca	aac	tac	ggc	gtt	gtg	1008
95	Lys	Ala	Phe	Phe	Arg	Val	Gly	Arg	Leu	Tyr	Ala	Asn	Tyr	Gly	Val	Val	
96			325						330				335				
97	gac	cag	gag	gcg	aag	ctc	ttc	acg	cta	aag	gaa	gcc	aag	gcg	gcg	acc	1056
98	Asp	Gln	Glu	Ala	Lys	Leu	Phe	Thr	Leu	Lys	Glu	Ala	Lys	Ala	Ala	Thr	
99			340					345				350					
100	gag	gcg	gcg	gcc	aag	acc	aag	tcc	acg	taa							1086
101	Glu	Ala	Ala	Ala	Lys	Thr	Lys	Ser	Thr								

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102          355          360
104 <210> SEQ ID NO: 2
105 <211> LENGTH: 361
106 <212> TYPE: PRT
107 <213> ORGANISM: Phytophthora infestans
109 <400> SEQUENCE: 2
110 Met Ala Thr Lvs Glu Ala Tyr Val Phe Pro Thr Leu Thr Glu Ile Lys
111 1          5          10          15
112 Arg Ser Leu Pro Lys Asp Cys Phe Glu Ala Ser Val Pro Leu Ser Leu
113          20          25          30
114 Tyr Tyr Thr Val Arg Cys Leu Val Ile Ala Val Ala Leu Thr Phe Gly
115          35          40          45
116 Leu Asn Tyr Ala Arg Ala Leu Pro Glu Val Glu Ser Phe Trp Ala Leu
117          50          55          60
118 Asp Ala Ala Leu Cys Thr Gly Tyr Ile Leu Leu Gln Gly Ile Val Phe
119 65          70          75          80
120 Trp Gly Phe Phe Thr Val Gly His Asp Ala Gly His Gly Ala Phe Ser
121          85          90          95
122 Arg Tyr His Leu Leu Asn Phe Val Val Gly Thr Phe Met His Ser Leu
123          100          105          110
124 Ile Leu Thr Pro Phe Glu Ser Trp Lys Leu Thr His Arg His His His
125          115          120          125
126 Lys Asn Thr Gly Asn Ile Asp Arg Asp Glu Val Phe Tyr Pro Gln Arg
127          130          135          140
128 Lys Ala Asp Asp His Pro Leu Ser Arg Asn Leu Ile Leu Ala Leu Gly
129 145          150          155          160
130 Ala Ala Trp Leu Ala Tyr Leu Val Glu Gly Phe Pro Pro Arg Lys Val
131          165          170          175
132 Asn His Phe Asn Pro Phe Glu Pro Leu Phe Val Arg Gln Val Ser Ala
133          180          185          190
134 Val Val Ile Ser Leu Leu Ala His Phe Phe Val Ala Gly Leu Ser Ile
135          195          200          205
136 Tyr Leu Ser Leu Gln Leu Gly Leu Lys Thr Met Ala Ile Tyr Tyr Tyr
137          210          215          220
138 Gly Pro Val Phe Val Phe Gly Ser Met Leu Val Ile Thr Thr Phe Leu
139 225          230          235          240
140 His His Asn Asp Glu Glu Thr Pro Trp Tyr Ala Asp Ser Glu Trp Thr
141          245          250          255
142 Tyr Val Lys Gly Asn Leu Ser Ser Val Asp Arg Ser Tyr Gly Ala Leu
143          260          265          270
144 Ile Asp Asn Leu Ser His Asn Ile Gly Thr His Gln Ile His His Leu
145          275          280          285
146 Phe Pro Ile Ile Pro His Tyr Lys Leu Lys Lys Ala Thr Ala Ala Phe
147          290          295          300
148 His Gln Ala Phe Pro Glu Leu Val Arg Lys Ser Asp Glu Pro Ile Ile
149 305          310          315          320
150 Lys Ala Phe Phe Arg Val Gly Arg Leu Tyr Ala Asn Tyr Gly Val Val
151          325          330          335
152 Asp Gln Glu Ala Lys Leu Phe Thr Leu Lys Glu Ala Lys Ala Ala Thr

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153          340          345          350
154 Glu Ala Ala Ala Lys Thr Lys Ser Thr
155          355          360
157 <210> SEQ ID NO: 3
158 <211> LENGTH: 25
159 <212> TYPE: DNA
160 <213> ORGANISM: Artificial
162 <220> FEATURE:
163 <223> OTHER INFORMATION: Primer
165 <400> SEQUENCE: 3
166 taagcttaca tggcgacgaa ggagg                25
169 <210> SEQ ID NO: 4
170 <211> LENGTH: 24
171 <212> TYPE: DNA
172 <213> ORGANISM: Artificial
174 <220> FEATURE:
175 <223> OTHER INFORMATION: Primer
177 <400> SEQUENCE: 4
178 tggatccact tacgtggast tggg                24
181 <210> SEQ ID NO: 5
182 <211> LENGTH: 24
183 <212> TYPE: DNA
184 <213> ORGANISM: Artificial
186 <220> FEATURE:
187 <223> OTHER INFORMATION: Primer
189 <400> SEQUENCE: 5
190 ctgggttcagg tgcattcgcc ggcg                24
192 <210> SEQ ID NO: 6
193 <211> LENGTH: 24
194 <212> TYPE: DNA
195 <213> ORGANISM: Artificial
197 <220> FEATURE:
198 <223> OTHER INFORMATION: Primer
200 <400> SEQUENCE: 6
201 gcggccgcat ggcgacgaag gagg                24

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RAW SEQUENCE LISTING ERROR SUMMARY      DATE: 09/05/2006  
PATENT APPLICATION: US/10/590,958      TIME: 15:09:04

Input Set : A:\Sequence Listing-13987-00019-US.txt  
Output Set: N:\CRF4\09052006\J590958.raw

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,  
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:3,4,5,6

**VERIFICATION SUMMARY**

**PATENT APPLICATION: US/10/590,958**

**DATE: 09/05/2006**

**TIME: 15:09:04**

**Input Set : A:\Sequence Listing-13987-00019-US.txt**

**Output Set: N:\CRF4\09052006\J590958.raw**

L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date